

In the specification:

Please amend the sentence beginning at page 1, line 13 as follows:

The present invention relates generally to plants that display altered structure or morphology and to the genes imparting such ~~phenotypes~~ phenotypes.

Please amend the sentence beginning at page 2, line 24 as follows:

Recently, Ephritikhine et al. (1999) reported that *hypersensitive to abscisic acid and auxin1 (sax1)* is defective in a step before ~~DET2~~DET2, but the *SAX1* gene has not yet been identified.

Please amend the paragraph beginning at page 7, line 3 as follows:

In another embodiment the invention is directed to a method for altering the biochemical activity of a cell comprising:

- (a) introducing at least one polynucleotide as described above into the cell; and
- (b) causing expression of said polynucleotide such that the biochemical activity of the cell is altered. The polynucleotide may be introduced into the cell ex vivo or in vivo.

In certain embodiments, the biochemical activity is selected from the group consisting of altered sterol Δ^7 reductase activity and altered sterol composition. Additionally, more than one *dwf5* polynucleotide may be provided to the cell.

Please amend the sentence beginning at page 12, line 1 as follows:

Details of these programs can be found at the National Center for Biotechnology Information's website. ~~the following internet address: <http://www.ncbi.nlm.gov/cgi-bin/BLAST>~~.

Please amend the sentence beginning at page 35, line 16 as follows:

For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to ~~chlorsulfuron~~ chlorsulfuron or Basta.

Please amend the sentence beginning at page 40, line 18 as follows:

~~Once~~ One class of analogs is those polypeptide sequences that differ from the native DWF5 polypeptide by changes, insertions, deletions, or substitution; at positions flanking the domain and/or conserved residues.

Please amend the sentence beginning at page 44, line 26 as follows:

Standard procedures for plant growth, measurements on floral organs, scoring the number of seeds in a silique, biochemical complementation tests with Brassinosteroids, analysis of endogenous Brassinosteroids, and ~~13C~~ ¹³C-labeled mevalonic acid feeding experiments have been described previously (~~Choe,~~ Choe, et al., 1999b).

Please amend the paragraph beginning at page 47, line 3 as follows:

dwf5 mutants are larger than ~~dwf4~~ *dwf4* in height with a concomitant increase in fertility. Among the *dwf5* mutants, *dwf5-2* and *dwf5-3* are the most severe.

Key characteristics of *dwf5* mutants include a short robust stature, short internodes, an increased number of inflorescences, and dark-green, round leaves similar to the phenotype previously reported for the other BR dwarfs (Azpiroz, et al., 1998; Choe, et al., 1999a, 1999b). The height of *dwf5* plants was variable depending on the allele (Table 1), ranging from 22 to 53% of wild-type height at 6 weeks of age. The lengths of the petioles, pedicels, and ~~siliques~~ siliques were also reduced in *dwf5* alleles.

Please amend the sentence beginning at page 49, line 16 as follows:

Unlike wild type, ¹³C-MVA was converted to ¹³C₅-7-dehydrocampesterol and ~~13C₅-7~~ ¹³C₅-7-dehydrocampestanol.

Please amend the paragraph beginning at page 50, line 18 as follows:

Experiments performed in support of the present invention (described above) indicated that the biosynthetic defect in *dwf5* lies at the S7R reaction. In view of these findings, DNA sequence databases (e.g., GenBank, National Center for Biotechnology Information (NCBI), Bethesda MD; see NCBI's website-<http://www.ncbi.nlm.nih.gov>) were searched for candidate

genes whose products were associated with the S7R reaction. An Arabidopsis S7R cDNA sequence was found in GenBank (Lecain, et al., 1996).

Please amend paragraph beginning at page 51, line 14 as follows:

In the primer designations the underlined space was used to distinguish forward or reverse primers from the gene acronym DW5, e.g., DWS 5R. Because only a cDNA sequence was available for S7R, possible exon-intron junctions were predicted before designing primers using the RNASPL utility available at the Baylor College of Medicine's website (Houston, TX).
~~;
http://www.hgsc.bcm.tmc.edu/SearchLauncher/~~.

Please amend sentence beginning at page 52, line 13 as follows:

Sequence analysis was performed using software packages, such as Genetics Computer Group (Madison, WI), DNASTAR (Madison, WI), and utilities available at the Arabidopsis website operated by Stanford University (~~http://genome~~ www.stanford.edu/Arabidopsis/).

Please amend Table 2 at page 53, line referring to *dwf5-1* as follows:

<i>dwf5-1</i>	2	Ws-2 ¹	T-DNA ²	single bp deletion (33423 ³)	elongated C-terminus (+44 aa)
---------------	---	-------------------	--------------------	--	-------------------------------

Please amend the sentence beginning at page 59, line 5 as follows:

It has been shown that the human steroid Δ^5 reductase gene expressed using the 35S promoter in ~~det2~~ det2 could complement the mutant phenotype, suggesting that the function of Δ^5 reductases are conserved between humans and Arabidopsis (Li and Chory, 1997).

Please amend paragraph beginning at page 61, line 6 as follows:

dwf5-1 contained a single base deletion (adenosine at 3343, numbered relative to the start codon; position 40123 of the sequence shown in Figure 7) near the stop codon (Figures 4A and 4B). The frameshift caused by this single base deletion is predicted to result in aberrant translation of 54 amino acids before the new stop codon. See the second row of amino acids corresponding to nucleotide positions 40136-4178 of Figure 7.